

RAW SEQUENCE LISTING

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Application Serial Number: 10/028,346
Source: FEW
Date Processed by STIC: 1-27-05

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/028,346

DATE: 01/27/2005

TIME: 16:07:27

Input Set : A:\15179.seq.txt

Output Set: N:\CRF4\01272005\J028346.raw

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3 <110> APPLICANT: Ong Abdullah, Meilina
4      Kulaveerasingam, Harikrishna
6 <120> TITLE OF INVENTION: A Molecular Marker
8 <130> FILE REFERENCE: 15179
10 <140> CURRENT APPLICATION NUMBER: 10/028,346
11 <141> CURRENT FILING DATE: 2001-12-20
13 <150> PRIOR APPLICATION NUMBER: AU PR2213
14 <151> PRIOR FILING DATE: 2000-12-20
16 <160> NUMBER OF SEQ ID NOS: 9
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 573
22 <212> TYPE: DNA
23 <213> ORGANISM: oil palm
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(573)
29 <400> SEQUENCE: 1
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32 1              5              10              15
34 acc acg cac ggg aag atc cgg atc cac gac tac gtc ggc gat ggt tgg      96
35 Thr Thr His Gly Lys Ile Arg Ile His Asp Tyr Val Gly Asp Gly Trp
36              20              25              30
38 gcc atc atc ttc tcc cat ccc gcg gat ttc aca ccc gtg tgc acg acg      144
39 Ala Ile Ile Phe Ser His Pro Ala Asp Phe Thr Pro Val Cys Thr Thr
40              35              40              45
42 gag ctg ggg aag atg gcg gcg tac gcg gag gag ttc gag aaa aga ggg      192
43 Glu Leu Gly Lys Met Ala Ala Tyr Ala Glu Glu Phe Glu Lys Arg Gly
44 50              55              60
46 gtg aag ctg cta ggc atc tcc tgc gac gat gtc aag tgc cac atg gaa      240
47 Val Lys Leu Leu Gly Ile Ser Cys Asp Asp Val Lys Cys His Met Glu
48 65              70              75              80
50 tgg atc aaa gac gtc gag gcc tac acg ccc gga tgt cgc gta aca tat      288
51 Trp Ile Lys Asp Val Glu Ala Tyr Thr Pro Gly Cys Arg Val Thr Tyr
52              85              90              95
54 cca att gta gcc gac ccc aag agg gag gtg atc aaa ctg ctg aac atg      336
55 Pro Ile Val Ala Asp Pro Lys Arg Glu Val Ile Lys Leu Leu Asn Met
56              100              105              110
58 gta gac cct gag gag aag gac tca aat ggg aac cag ctc ccg tca cgg      384
59 Val Asp Pro Glu Glu Lys Asp Ser Asn Gly Asn Gln Leu Pro Ser Arg
60              115              120              125
62 gcc ctt cat ata gtg ggc cct gat aag aag gtt aag ctg agc ttt ctg      432

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63 Ala Leu His Ile Val Gly Pro Asp Lys Lys Val Lys Leu Ser Phe Leu
64      130      135      140
66 tac ccg gcg tcg acg ggg cgg aac atg gag gag gtg gtc agg gtg ttg      480
67 Tyr Pro Ala Ser Thr Gly Arg Asn Met Glu Glu Val Val Arg Val Leu
68 145      150      155      160
70 gag tcg ctt cag aag acg atc aag tat aag gtg gcg acc cca gcg aac      528
71 Glu Ser Leu Gln Lys Thr Ile Lys Tyr Lys Val Ala Thr Pro Ala Asn
72      165      170      175
74 tgg aaa ccg ggg gag ccg gtg gtg atc tcg ccc gag cgt gtc caa      573
75 Trp Lys Pro Gly Glu Pro Val Val Ile Ser Pro Glu Arg Val Gln
76      180      185      190
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79 <211> LENGTH: 191
80 <212> TYPE: PRT
81 <213> ORGANISM: oil palm
83 <400> SEQUENCE: 2
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87 Thr Thr His Gly Lys Ile Arg Ile His Asp Tyr Val Gly Asp Gly Trp
88      20      25      30
90 Ala Ile Ile Phe Ser His Pro Ala Asp Phe Thr Pro Val Cys Thr Thr
91      35      40      45
93 Glu Leu Gly Lys Met Ala Ala Tyr Ala Glu Glu Phe Glu Lys Arg Gly
94      50      55      60
96 Val Lys Leu Leu Gly Ile Ser Cys Asp Asp Val Lys Cys His Met Glu
97 65      70      75      80
99 Trp Ile Lys Asp Val Glu Ala Tyr Thr Pro Gly Cys Arg Val Thr Tyr
100      85      90      95
102 Pro Ile Val Ala Asp Pro Lys Arg Glu Val Ile Lys Leu Leu Asn Met
103      100      105      110
105 Val Asp Pro Glu Glu Lys Asp Ser Asn Gly Asn Gln Leu Pro Ser Arg
106      115      120      125
108 Ala Leu His Ile Val Gly Pro Asp Lys Lys Val Lys Leu Ser Phe Leu
109      130      135      140
111 Tyr Pro Ala Ser Thr Gly Arg Asn Met Glu Glu Val Val Arg Val Leu
112 145      150      155      160
114 Glu Ser Leu Gln Lys Thr Ile Lys Tyr Lys Val Ala Thr Pro Ala Asn
115      165      170      175
117 Trp Lys Pro Gly Glu Pro Val Val Ile Ser Pro Glu Arg Val Gln
118      180      185      190
120 <210> SEQ ID NO: 3
121 <211> LENGTH: 873
122 <212> TYPE: DNA
123 <213> ORGANISM: oil palm
125 <220> FEATURE:
126 <221> NAME/KEY: CDS
127 <222> LOCATION: (28)..(600)
129 <400> SEQUENCE: 3
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131                               Met Pro Gly Leu Thr Ile Gly Asp Thr
132                               1           5
134 atc ccg aac ctg gag gtg gag acc acg cac ggg aag atc cgg atc cac      102
135 Ile Pro Asn Leu Glu Val Glu Thr Thr His Gly Lys Ile Arg Ile His
136 10                               15           20           25
138 gac tac gtc ggc gat ggt tgg gcc atc atc ttc tcc cat ccc gcg gat      150
139 Asp Tyr Val Gly Asp Gly Trp Ala Ile Ile Phe Ser His Pro Ala Asp
140                               30           35           40
142 ttc aca ccc gtg tgc acg acg gag ctg ggg aag atg gcg gcg tac gcg      198
143 Phe Thr Pro Val Cys Thr Thr Glu Leu Gly Lys Met Ala Ala Tyr Ala
144                               45           50           55
146 gag gag ttc gag aaa aga ggg gtg aag ctg cta ggc atc tcc tgc gac      246
147 Glu Glu Phe Glu Lys Arg Gly Val Lys Leu Leu Gly Ile Ser Cys Asp
148                               60           65           70
150 gat gtc aag tgc cac atg gaa tgg atc aaa gac gtc gag gcc tac acg      294
151 Asp Val Lys Cys His Met Glu Trp Ile Lys Asp Val Glu Ala Tyr Thr
152                               75           80           85
154 ccc gga tgt cgc gta aca tat cca att gta gcc gac ccc aag agg gag      342
155 Pro Gly Cys Arg Val Thr Tyr Pro Ile Val Ala Asp Pro Lys Arg Glu
156 90                               95           100          105
158 gtg atc aaa ctg ctg aac atg gta gac cct gag gag aag gac tca aat      390
159 Val Ile Lys Leu Leu Asn Met Val Asp Pro Glu Glu Lys Asp Ser Asn
160                               110          115           120
162 ggg aac cag ctc ccg tca cgg gcc ctt cat ata gtg ggc cct gat aag      438
163 Gly Asn Gln Leu Pro Ser Arg Ala Leu His Ile Val Gly Pro Asp Lys
164                               125          130           135
166 aag gtt aag ctg agc ttt ctg tac ccg gcg tgc acg ggg cgg aac atg      486
167 Lys Val Lys Leu Ser Phe Leu Tyr Pro Ala Ser Thr Gly Arg Asn Met
168                               140          145           150
170 gag gag gtg gtc agg gtg ttg gag tgc ctt cag aag acg atc aag tat      534
171 Glu Glu Val Val Arg Val Leu Glu Ser Leu Gln Lys Thr Ile Lys Tyr
172                               155          160           165
174 aag gtg gcg acc cca gcg aac tgg aaa ccg ggg gag ccg gtg gtg atc      582
175 Lys Val Ala Thr Pro Ala Asn Trp Lys Pro Gly Glu Pro Val Val Ile
176 170                               175          180           185
178 tcg ccc gag cgt gtc caa tgaggaggcc aagcagatgt tcccgcaggg      630
179 Ser Pro Glu Arg Val Gln
180                               190
182 agttgagaat gtgaatctcc catcgaagaa ggattacctc cgcttcacaa aagtctaag      690
184 ttgttgggcc gtccgtgata tggttcataag tggtttctgg ggcccactg tatactgtgt      750
186 tgtcgtgtta tatgtttgtg ttggtatcat gtagtttgtg ccttagggga gtttggatat      810
188 taattttag tagttatgttaa ttattaaagt ttttaccatg agattaaaaa aaaaaaaaaa      870
190 aaa
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 191
194 <212> TYPE: PRT
195 <213> ORGANISM: oil palm
197 <400> SEQUENCE: 4
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199 1          5          10          15
201 Thr Thr His Gly Lys Ile Arg Ile His Asp Tyr Val Gly Asp Gly Trp
202          20          25          30
204 Ala Ile Ile Phe Ser His Pro Ala Asp Phe Thr Pro Val Cys Thr Thr
205          35          40          45
207 Glu Leu Gly Lys Met Ala Ala Tyr Ala Glu Glu Phe Glu Lys Arg Gly
208          50          55          60
210 Val Lys Leu Leu Gly Ile Ser Cys Asp Asp Val Lys Cys His Met Glu
211 65          70          75          80
213 Trp Ile Lys Asp Val Glu Ala Tyr Thr Pro Gly Cys Arg Val Thr Tyr
214          85          90          95
216 Pro Ile Val Ala Asp Pro Lys Arg Glu Val Ile Lys Leu Leu Asn Met
217          100          105          110
219 Val Asp Pro Glu Glu Lys Asp Ser Asn Gly Asn Gln Leu Pro Ser Arg
220          115          120          125
222 Ala Leu His Ile Val Gly Pro Asp Lys Lys Val Lys Leu Ser Phe Leu
223          130          135          140
225 Tyr Pro Ala Ser Thr Gly Arg Asn Met Glu Glu Val Val Arg Val Leu
226 145          150          155          160
228 Glu Ser Leu Gln Lys Thr Ile Lys Tyr Lys Val Ala Thr Pro Ala Asn
229          165          170          175
231 Trp Lys Pro Gly Glu Pro Val Val Ile Ser Pro Glu Arg Val Gln
232          180          185          190
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235 <211> LENGTH: 17
236 <212> TYPE: DNA
237 <213> ORGANISM: oil palm
239 <400> SEQUENCE: 5
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242 <210> SEQ ID NO: 6
243 <211> LENGTH: 18
244 <212> TYPE: DNA
245 <213> ORGANISM: oil palm
247 <400> SEQUENCE: 6
248 caaactctca gctaggca
250 <210> SEQ ID NO: 7
251 <211> LENGTH: 218
252 <212> TYPE: PRT
253 <213> ORGANISM: Hordeum vulgare
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260          20          25          30
262 Val Ile Leu Phe Ser His Pro Gly Asp Phe Thr Pro Val Cys Thr Thr
263          35          40          45
265 Glu Leu Ala Ala Met Ala Asn Tyr Ala Lys Glu Phe Glu Lys Arg Gly
266          50          55          60
268 Val Lys Leu Leu Gly Ile Ser Cys Asp Asp Val Gln Ser His Lys Glu

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17

18

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269 65          70          75          80
271 Trp Thr Lys Asp Ile Glu Ala Tyr Lys Pro Gly Ser Lys Val Thr Tyr
272          85          90          95
274 Pro Ile Met Ala Asp Pro Asp Arg Ser Ala Ile Lys Gln Leu Asn Met
275          100          105          110
277 Val Asp Pro Asp Glu Lys Asp Ala Gln Gly Gln Leu Pro Ser Arg Thr
278          115          120          125
280 Leu His Ile Val Gly Pro Asp Lys Val Val Lys Leu Ser Phe Leu Tyr
281          130          135          140
283 Pro Ser Cys Thr Gly Arg Asn Met Asp Glu Val Val Arg Ala Val Asp
284 145          150          155          160
286 Ser Leu Leu Thr Ala Ala Lys His Lys Val Ala Thr Pro Ala Asn Trp
287          165          170          175
289 Lys Pro Gly Glu Cys Val Val Ile Ala Pro Gly Val Ser Asp Glu Glu
290          180          185          190
292 Ala Lys Lys Met Phe Pro Gln Gly Phe Glu Thr Ala Asp Leu Pro Ser
293          195          200          205
295 Lys Lys Gly Tyr Leu Arg Phe Thr Lys Val
296          210          215
298 <210> SEQ ID NO: 8
299 <211> LENGTH: 216
300 <212> TYPE: PRT
301 <213> ORGANISM: Arabidopsis thaliana
303 <400> SEQUENCE: 8
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308          20          25          30
310 Thr Val Leu Phe Ser His Pro Gly Asp Phe Thr Pro Val Cys Thr Thr
311          35          40          45
313 Glu Leu Gly Ala Met Ala Lys Tyr Ala His Glu Phe Asp Lys Arg Gly
314          50          55          60
316 Val Lys Leu Leu Gly Leu Ser Cys Asp Asp Val Gln Ser His Lys Asp
317 65          70          75          80
319 Trp Ile Lys Asp Ile Glu Ala Phe Asn His Gly Ser Lys Val Asn Tyr
320          85          90          95
322 Pro Ile Ile Ala Asp Pro Asn Lys Glu Ile Ile Pro Gln Leu Asn Met
323          100          105          110
325 Ile Asp Pro Ile Glu Asn Gly Pro Ser Arg Ala Leu His Ile Val Gly
326          115          120          125
328 Pro Asp Ser Lys Ile Lys Leu Ser Phe Leu Tyr Pro Ser Thr Thr Gly
329          130          135          140
331 Arg Asn Met Asp Glu Val Leu Arg Ala Leu Asp Ser Leu Leu Met Ala
332 145          150          155          160
334 Ser Lys His Asn Asn Lys Ile Ala Thr Pro Val Asn Trp Lys Pro Asp
335          165          170          175
337 Gln Pro Val Val Ile Ser Pro Ala Val Ser Asp Glu Glu Ala Lys Lys
338          180          185          190
340 Met Phe Pro Gln Gly Phe Lys Thr Ala Asp Leu Pro Ser Lys Lys Gly

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VERIFICATION SUMMARY

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